

**AMENDMENTS TO THE SPECIFICATION**

Please replace paragraph [00032] with the following paragraph:

[00032] The method of the present invention has improved efficacy over the previously described methods, *i.e.* it has been shown to provide remarkably reliable predictions (*see* Fig. 8 and Example 1, *infra*) (SEQ ID NO: 128) and it is generally applicable to all biopolymers, including, *inter alia*, RNA, DNA and proteins (*see* Figs. 8-11 and Examples 1-4, *infra*). In particular, the present invention demonstrates improved efficacy over the previously describe methods partly due to: 1) a scoring process that results in scores that are symmetric and uniformly scaled, and/or a process of standardization that results in scores that are uniformly scaled; 2) a rigorous screening process that is intricately linked to its scoring algorithms, such that high accuracy is achieved; 3) a screening process that is neither arbitrary nor absolute, and thus able to implicitly handle the effects of sequence selection, phylogenetic relationships, sequence number; 4) a methodology that does not require preconceived biochemical parameters, or any other type of empirical data such as physicochemical, energetic, similarity descriptors or matrixes and is thus unbiased and not rule-based; 5) a methodology that is highly automated, and does not require enormous amounts of user input; 6) a methodology for evaluating the quality of the input data and suggestion for how to improve it, and is thus a novel method by which to analyze sequence alignments for errors; and 7) a methodology that is iterative, because as the input data is refined via its misalignment algorithm, each successive pass allows for better predictions.

Please replace paragraph [00041] with the following paragraph:

[00041] Figure 8(a) shows the structure for Domain V of the Group II catalytic RNA AI5 $\gamma$  as predicted by the exemplary embodiment of the method of the present invention (SEQ ID NO: 128) and 8(b) shows the interactions for Domain V of the Group II catalytic RNA AI5 $\gamma$  according to the biochemically predicted structure (SEQ ID NO: 128);

Please replace paragraph [00046] with the following paragraph:

[00046] Shevek: An exemplary embodiment of the method of the present invention described ~~hereinbelow~~ herein below.

Please replace paragraph [00128] with the following paragraph:

[00128] The steps of the above-described method are preferably performed by a computer. In one preferred embodiment, the computer is a Dell Precision 430 dual processor Pentium III™, 933 [[Mz]] MHz Workstation. Use of the sequence alignment editor software, Se-Al, may be performed on a Power Macintosh 8600/300 Power PC. When the method is performed by a computer, the above-described method steps are embodied in a program storage device readable by a machine, such program storage device including a computer readable medium. Computer readable media include magnetic diskettes, magnetic tapes, optical disks, Read Only Memory, RAM, Direct Access Storage Devices, gate arrays, electrostatic memory, and any other like medium.

Please replace paragraph [00141] with the following paragraph:

[000141] Four sequences were identified as misaligned. These sequences were inspected and edited using the sequence alignment editor program Se-Al, as described previously. [Sequences #43 SEQ ID NO:44 ( ZPU16993\_cox2) and SEQ ID NO:53 ( BVSCOXII1\_cox2\_1) were noted to be misaligned and realigned (see Table X). ~~Sequence #16~~ SEQ ID NO:17 (DRP130746\_Dp\_nad5) and ~~sequence #73~~ SEQ ID NO:74 (petB\_45\_) were noted to be unusual, but not in need of realignment.] The entire Shevek process was then repeated on the altered sequence alignment data set i.e. the process was iterated.

Please replace Table 1 at page 53 with the following table:

TABLE I  
Sequence Alignment Data

	<u>POSITION</u>																								
	0	2	4	6	8	1	1	1	1	1	2	2	2	2	2	3	3	3	3	3	4	4	4	4	4
	0	2	4	6	8	0	2	4	6	8	0	2	4	6	8	0	2	4	6	8	0	2	4	6	8
<u>Sequence of Interest:</u>																									
ai5gamma	----GAGCCGTATGCGAT-----GAAA-----GTCGCACGTACGGTTC--T																								
<u>Functionally Related Sequences:</u>																									
MICLURF1_ndh1__01_	----GAGCCACATGCAGG-----GAAA-----CTTGCAAGTGTGGTTC--T																								
_MIZMCO_cox2_1__02_	----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTCAAGTTT--G																								
_DCCOXII_cox2_1	----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTACAGTTT--G																								
_MITACOII_cox2_1	----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTCAAGTTT--G																								
MIPHC021_cox2_1	----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTACAGTTT--G																								
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_MIOS01_Os_cox2	---GAGCTTTTTGCGGG---GAAA---CTTGCAAGTAAAGTTT--G	<u>7</u>
_MIHACOXII_cox2	---GAGCTTTTTGCGGG---GAAA---CTTGCAAGTACAGTTT--G	<u>8</u>
_MIDBG2IA_nad5_1_03_	---GAGCCGTGTGATGG---GAAA---CCTTCCCGCACGGTTC--G	<u>9</u>
_MTVFNAD5_nad5_1	---GAGCCGTGTGATGG---GAAA---CCTTCCCGCACGGTTC--G	<u>10</u>
MIATNAD5A_nad5_1	---GAGCCGTGTGATGG---GAAA---CCTTCCCGCACGGTTC--G	<u>11</u>
TSP131146_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>12</u>
TRA131145_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>13</u>
ASP130735_Sc_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>14</u>
SAU131147_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>15</u>
AEV130737_Ap_nad5	---GAGCCGTATGCGGG---GAAA---CTTGACAGTGCAGTTT--T	<u>16</u>
DPR130746_Dp_nad5	---GAGCCGTATGCGAA---GAAA---CTTGACAGTGCAGTTT--T	<u>17</u>
ANNAD5_An_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>18</u>
DSP130747_Dd_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>19</u>
SWI131144_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>20</u>
AF143422_Tc_nad5	---GAGCCGTGTGATGG---GAAA---CCTCCCGCACGGTTC--G	<u>21</u>
AF143423_Pa_nad5	---GAGCCGTGTGATGG---GAAA---CCTCCCGCACGGTTC--G	<u>22</u>
AF143424_Ca_nad5	---GAGCCGTGTGATGG---GAAA---CCTCCCGCACGGTTC--G	<u>23</u>
AF143425_Cp_nad5	---GAGCCGTGTGATGG---GAAA---CCTCCCGCACGGTTC--G	<u>24</u>
MTPACG_nad5_4_08_	---GAGCCGTATGATGG---GAAA---CTATCACGTACGGTTC--G	<u>25</u>
MIATGENA_nad7_1	---TGAGCGCATGCGGG---GAGA---CCCGCACGTACGGTTT--T	<u>26</u>
MIATGENA_nad7_3	---GAGCCGTATGAAGG---GAAA---CTCTCACGTACAGTTT--G	<u>27</u>
_MPOMTCG_nad3	---GAGCCGTGTAATGG---GCAA---CTATTTTCGCACGGTTC--G	<u>28</u>
MIATGENA_nad4_3	---GAGCCTAGTGATAG---GAGA---CTATCTAGCTTGGTTC--G	<u>29</u>
_MPOMTCG_nad4	---GAGCCGTATGCGAG---GAGA---CTTGACAGTACGGTTC--G	<u>30</u>
MISC13_cox1_1_04_	---AAGCCGTATGATGG---GAAA---CTATCACGTACGGTTT--G	<u>31</u>
MTPACG_cox1_1_07_	---GAGCCGTATGCGGT---GAAA---GTCGCACGTACGGTTC--G	<u>32</u>
MTPCCOX1_cox1_1	---GAGCCGTATGCGGT---GAAA---GTCGCACGTACGGTTC--G	<u>33</u>
SPO251292_cox1_1	---GAGCCGTATGCATT---GAAA---GATGCACGTACGGTTC--T	<u>34</u>
MIKLCOX1_cox1_1	---GAGCCGTATGATAT---GAAA---GTATCACGTACGGTTC--G	<u>35</u>
MISC13_cox1_2_05_	---GAGCCGTATGATAT---GAAA---GTATCACGTACGGTTC--G	<u>36</u>
MTPACG_cox1_4_06_	---GAGCCGTATGCAGG---GAAA---CTTGACAGTACGGTTC--G	<u>37</u>
AMU41288_Am_cox1_3	---GAGCCGTATGCGGT---GAAA---GTTGCACGTACGGTTC--G	<u>38</u>
MISPCG_cob_09_	---GAGCCGTATAATTA---CGAAA---GTATCCCGTACGGTTC--G	<u>39</u>
CHNTHX_rps12_10_	---AAGCCGTATTTCGAT---GAAA---GTCGTATGTACGGCTT--G	<u>40</u>
CHSORPS_rps12_2_11_	---AAGCCGTATTTCGAT---GAAA---GTCGTATGTACGGCTT--G	<u>41</u>
CHZMXX_rps12_2_12_	---AAGCCGTATTTCGAT---GAAA---GTCGTATGTACGGCTT--G	<u>42</u>
CHMPXX_rps12_2_13_	---AAGCCGTATTTCGTT---GAAA---ATCGGATGTACGGTTT--G	<u>43</u>
_ZPU16993_cox2	---GAGCTTTTTGCGGG---GAAA---CTTGCAAGTCAAGTTT--G	<u>44</u>
AF080087_Ot_rps3	---GAGCCGTGTGATGG---GTGA---CTATCCAGCACGGTTC--G	<u>45</u>
CHNTHX_trnI_14_	---GAGCGCAGTACAAC---GGAGA---GTTGTATGCTGCGTTC--G	<u>46</u>
CHZMXX_trnI_15_	---GAGCGCAGTACAAC---GGGGA---GTTGTATGCTGCGTTC--G	<u>47</u>
CHMPXX_trnI_16_	---GAGCGCAGTACAAC---GGAAA---GTTGTATGCTGCGTTC--G	<u>48</u>
WHTCPTRNI_trnI	---GAGCGCAGTACAAC---GGGGA---GTTGTATGCTGCGTTC--G	<u>49</u>
CHNTHX_trnA_17_	---GAGCACAGTACGAT---GAAA---GTTGTAAGCTGTGTTC--G	<u>50</u>
CHZMXX_trnA_18_	---GAGCACAGTACGAT---GAAA---GTTGTAAGCTGTGTTC--G	<u>51</u>
CHMPXX_trnA_19_	---GAGCACAGTACGAT---GAAA---GTTGTAAGCTGTGTTC--G	<u>52</u>
_BVSCOXIII_cox2_1	---GAGCTTTTTGCGGG---GAAA---CTTGCAAGTACAGTTT--G	<u>53</u>
CHNTHX_trnK_26_	---AAGCCGTGTGCAAT---GAAA---AATGCAAGCACGGCTT--G	<u>54</u>
CHSATRNK_trnK_27_	---AAGCTGTGTGCAAT---GAAA---AATGCAAGCACGGTTT--G	<u>55</u>

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CHMPXX_trnK_28_	----AAGCCGTATGCAGT----	AAAA----	ATTGCAAGTACGGTTT--G	56
CHNTXX_atpF_29_	----GAGCCAAATGAATC----	GAAA----	GATTCATGTTTGGTTC--G	57
CHPSATPC_atpF_30_	----GAGCCAAATGAATT----	GAAA----	GATTCATGTTTGGTTC--G	58
SOL400848_atpF_31_	----GAGCCAAATGAATT----	GAAA----	AATTCACGTTTGGTTC--G	59
CHTAATP1_atpF_32_	----GAGCCAAATGAATC----	GAAA----	GATTCATGTTTGGTTC--G	60
CHMPXX_atpF_33_	----AAGCCGAATGAATT----	GAAA----	AGTTCATGTTTCGGTTT--G	61
HVU010573_atp9_	----GAGCCAAATGAATC----	GAAA----	GATTCATGTTTGGTTC--G	62
CHNTXX_rpl2_34_	----AAGAAGTATGCTTT----	GGAA----	GAAGCTTGACAGTTT--G	63
CHMPXX_Cp_rpl2_	----AAGCTGTATGCTT----	GAAA----	AAAGCTTGACAGTTT--G	64
MIATGENA_rpl2_1_	----GAGCCGTACGAG----	GCAG----	CTCACGTACGGTTC--G	65
SCE011856_cytB_37_	----GAGCTGTATACTAT----	GAAA----	GTAGTACGTACAGTTC--T	66
CHNTXX_rps16_38_	----GAGCCGTACGAGGA----	GAAA----	GCTTCCTATACGTTTC--T	67
CHNTXX_rpoC1_39_	----GAGCCGGATGAAAG----	GAAA----	CTTTCACGTCCGATTT--T	68
SOL400848_rpoC1_40_	----GAGCCGGGCGAGGG----	GAAA----	CTTTCACGTCCGGCTT--T	69
CHMPXX_rpoC1_41_	----GAGCCGGATGACGG----	AAAA----	CTTTCATGTCCGATTC--T	70
CHMPXX_orf135_42_	----AAGCCATACAGAGTT----	GAAA----	ATATCATATATGGTTT--T	71
CHNTXX_petB_43_	----GAGCTGTACGAGAT----	GAAA----	GTCTCATATACGGTTC--T	72
SOL400848_petB_44_	----GAGCTGTACGAGAT----	GAAA----	GTCTCATATACAGTTC--T	73
CHZMXX_petB_45_	----GAGCCGTACGAGAT----	GAAA----	TTTTCATATACGGTTC--	74
CHMPXX_petB_46_	----AAGCTGTAAGATTA----	TAAA----	TAATCATTTACGGTTT--T	75
CHNTXX_petD_47_	----GAGCTGGATGATTA----	AAAA----	TTATCATGTCCAGTTC--C	76
SOL400848_petD_48_	----GAGCCGGATGATGA----	AAAA----	TTATCATGTCCGGTTC--T	77
CHZMXX_petD_49_	----GAGCCGGATGATGAA----	AAA----	TTCTCATGTCCGGTTC--C	78
CHMPXX_petD_50_	----GAGCCGGATGATAT----	TAAA----	TTATCATGTCCGATTC--T	79
CHNTXX_clpP_1_51_	----GAACCGTATGCATC----	AAAA----	GGCGCATGTACGGTTC--C	80
CHMPXX_clpP_1_52_	----AAGCTGTATGCGCTT----	AAAA----	AGTGCTTGACAGTTT--T	81
CHNTXX_ycf3_2_53_	----GAGCCGTATGAGGT----	AAGAAA----	TTCTCAAGTACGGTTC--T	82
CHNTXX_rpl16_54_	----GAGCTGGATGAGAA----	GAAA----	CTCTCACGTCCGGTTC--T	83
CHZMXX_rpl16_55_	----GAGCTGGATGAGAA----	GAAA----	CTCTCATGTCCAGTTT--T	84
CHSOL16_rpl16_56_	----GAGCCGGATGAGAA----	GAAA----	CTCTCATGTCCGGTTC--T	85
CHMPXX_rpl16_57_	----GAGCCGGATGAAT----	CAAAA----	TTTCATGTCCGGTTT--T	86
CHNTXX_ndh1_58_	----GAGCCGTATGAGAT----	GAAA----	ATCTCACGTACGGTTC--T	87
CHMPXX_ndh1_59_	----GAGCCGTATGAAAT----	GAAA----	ATTTTCATGTACGGTTT--T	88
CHNTXX_ndh2_60_	----GAGCCGTGTGAGAT----	GAAA----	GTCTCATGCACGGTTT--T	89
CHMPXX_ndh2_61_	----GAGCCGTGTGAATT----	GAAA----	ATCTCATGCACGGTTT--T	90
OBENAD202_nad2_4_	----GAGCCGTATGATGG----	GCAA----	CTATCTCCTGCGGTTC--G	91
CHNTXX_ycf3_1_62_	----GAGCCGTATGAGGT----	GAAA----	ATCTCACGTACGGTTC--T	92
CHMPXX_ycf3_1_63_	----GAGCCGTATGAAGT----	TTAA----	ACTTCATGTACGGTTT--T	93
__CHNTXX_trnG_64_	----GAGCCGAATGAAAC----	CAAA----	GTTTCATGTTTCGGTTT--T	94
__CHTATRN1_trnG_65_	----GAGCCGAATGAAAT----	CAAA----	ATTTTCATGTTTCGGTTT--T	95
__CHMPXX_trnG_66_	----GAGCCGAATGAAAG----	AAAA----	CTTTCACGTTCGGTTT--T	96
__MPOMTCG_trnG_	----GAGCCGGATGAGGGA----	GAAA----	TTTCTCACGTCCGGATC--T	97
CHNTXX_rps12_1_67_	----GAGCCGTATGAGGT----	GAAA----	ATCTCATGTACGGTTC--T	98
CHMPXX_rps12_1_68_	----AAGCCGTATGAAAT----	GAAA----	ATATCAAGTACGGTTT--T	99
CHZMXX_rps12_1_69_	----GAGCCGTATGAGGT----	GAAA----	ATCTCATGTACGGTTC--T	100
AMU41288_Am_rnl_	----GAGCCGTATGCGAT----	GAAA----	GTTGCACGTACGGTTC--T	101
AF029891_Cp_srRNA1	----GAGCCGTATGCGAT----	GAAA----	GTCGCACGTACGGTTC--T	102
TPSSRA_ssRNA	----GAGCCGTATGCGAT----	GAAA----	GTTGCACGTACGGTTC--T	103
AF087656_Aa_srRNA	----GAGCTGTATGCGAT----	GAAA----	GTCGCACGTACAGTTC--T	104

AF029891Cp_srRNA2	----GAGCCGTATGCCAT-----GAAA----GTGGCACGTACGGTTC--T	<u>105</u>
PLRRNA23_lrn_1	----CAGCCGTGTGCGGT-----GAAA----GTCGCACGCACGGTTG--T	<u>106</u>
PLRRNA23_lrn_2	----GAGCCGTGTGCGAT-----GAAA----GTCGCAAGCACGGTTC--T	<u>107</u>
PLRRNA23_lrn_3	----GAGCCGTGTGCGTT-----GAAA----GATGCATGCACGGTTC--T	<u>108</u>
PLRRNA23_lrn_4	----GAGCCGTATGAATG-----GAGA----CATTCACGTACGGTTT--T	<u>109</u>
MISOLSUR_rns2	----GAGCCGTGTGCGGT-----GAAA----GTCGCATGCACGGTTC--T	<u>110</u>
MPOMTCG_trnS	----GAGCCGTATGCGG-----GAAAA--CTCGCACGTACGGTTC--T	<u>111</u>
Azotobacter_Av_groEL	----GAGCCGTATGCGGG-----GAAA----CTCGCACGTACGGTTC--T	<u>112</u>
AF065404_Ba_pX01	----GAGCCGTATGTGCT-----GAAA----GGTACAAGTACGGTTC--	<u>113</u>
AB011549_Ec_IntE	----GAGCCGTATGCCGG-----GAAA----CTGGCACGTACGGTTC--T	<u>114</u>
PSY18999_Pp_Int5041C	----GAGCCGGATGAGGG-----GCCA--CTCTCATGTCCGGTTC--T	<u>115</u>
ECHREP_Ec_IntB	----GAGCGGTATGAGCC-----GAGA--GGTTCACGTACCGTTC--T	<u>116</u>
RMREVTM_Rm_Int1	----GAGCGGTGTGAATC-----GAGA--GGTTCACGCACCGTTC--T	<u>117</u>
ASU13767_An_hlyA	----GAGCCGTGTGCAGC-----GAAA--GTTGCACGCACGGATC--T	<u>118</u>
p	----GAGCCGTATGAGGT-----GAAA--GTCTCAAGTACGGTTT--T	<u>119</u>
LLU50902_Ll_ltrB	----GAGCCGTATACTCC-----GAGA--GGGGTACGTACGGTTC--C	<u>120</u>
PAU77945_Pa_Xin6	----CCGCCGTGTACG-----GAAC--CGTACGCACGGTGG--T	<u>121</u>
CDIIORF_Cd_orf14	----ACGCCGTGTGAGGG-----GAAA--CTCTCATGCACGGTGT--G	<u>122</u>
AB022308_Bm_TnpR	----ACGCCGTATGCTG-----GAAA--CTCGCCTGTACGGTGT--G	<u>123</u>
MTPLCOX1_cox1_1	----AAGCCGTATGAGGG-----GAAA--CTTTCACGTACGGTTT--G	<u>124</u>
MTPLCOX1_cox1_2	----GAGCCGTATGATGG-----GAAA--CTATCACGTACGGTTC--T	<u>125</u>
MTPLCOX1_cox1_3	----GAGCCCGGTGCGGT-----GAAA--GTCGCACGCCGGGTTC--G	<u>126</u>
SFU97489_Sf_IntA	----GAGCCGGATGCGCT-----GAAA--GGTGCACGTCCGGTTC--G	<u>127</u>

Please replace Table X at page 70 with the following table:

TABLE X  
Corrected Sequence Information

**Reference:**

**Sequence ID Number 1:**

AI5gamma                    ----GAGCCGTATGCGAT-----GAAA----GTCGCACGTACGGTTC--T

**Sequence ID Number [[43]] 44:**

*Before:*

\_ZPU16993\_cox2            -----GAGCTTTTGTGCGG----GAAA----CTTGCAAGTCAAGTTT--G

*After:*

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\_ZPU16993\_cox2 ----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTCAAGTTT--G

Sequence ID Number [[52]] 53:

*Before:*

\_BVSCOXIII1\_cox2\_1 -----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTACAGTTT--G

*After:*

\_BVSCOXIII1\_cox2\_1 ----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTACAGTTT--G